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(54) Title: CAROTENOID-ASSOCIATED PROTEINS USEFUL FOR HIGH CAROTENOID ACCUMULATION AND PRODUCTION IN PLANTS AND OTHER ORGANISMS (57) Abstract A method for production of high amounts of carotenoids in plants, bacteria or cells. Carotenoid-associated proteins CHRC and CHRD isolated from corollas of <i>Cucumis sativus</i> , <i>chrc</i> gene, CHRC deduced sequence, the molecular cloning, cDNA and RNA. A new CHRC promoter able to direct expression for foreign genes. The cloned promoter comprising approximately 3.5 kb of the CHRC upstream region.		

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CAROTENOID-ASSOCIATED PROTEINS USEFUL FOR HIGH CAROTENOID ACCUMULATION AND PRODUCTION IN PLANTS AND OTHER ORGANISMS

BACKGROUND OF THE INVENTION

Field of Invention

This invention concerns a method for production of high amounts of carotenoids in plants. In particular, the invention concerns carotenoid-associated proteins CHRC and CHRD isolated from corollas of *Cucumis sativus*, CHRC deduced sequence, the molecular cloning, cDNA, RNA and a homologous gene involved in expression of CHRC. The *Cucumis sativus* corollas proteins were found to be involved and to regulate carotenoid accumulation and sequestration in chromoplasts. Invention additionally concerns a new CHRC promoter able to direct expression of foreign genes. The cloned promoter comprises approximately 3.5 kb of the CHRC upstream region.

BACKGROUND ART AND RELATED ART DISCLOSURES

Carotenoids are very important dietary components in animals and are also important for plants as they are essential for plant photosynthesis. In humans, they are essential dietary components, which possess anticancer activity and protect against heart and age related diseases. Commercially, they are used to color food products. In flowers and plants they are responsible for their pigmentation. In photosynthetically active organisms, carotenoids are essential to the proper functioning of the light-harvesting apparatus and they determine color of fruits and flowers. Moreover, carotenoid synthetic pathway leads to the synthesis of key growth regulators.

In plants, carotenoids are accumulated in high amounts chromoplasts, carotenoid-containing plastids responsible for the yellow, orange and red colors of petals, fruits and some roots in various plant species. Information on the structural organization of chromoplasts comes mainly from studies of ripening processes in fruits [Plant Sci.

94:1-17 (1983)]. The disappearance of chlorophyll and accumulation of carotenoids have been shown to parallel fruit maturation. Following the chloroplast to chromoplast conversion thylakoid membranes disintegrate, most of the components of the photosynthetic machine disappear, and a new set of proteins accumulates instead. In pepper fruits containing fibrillar chromoplasts, two very abundant proteins with approximate molecular masses of 35 kDa (ChrB) and 58 kDa (ChrA) have been identified as chromoplast-specific [Plant Mol. Biol. 21:549-554 (1993)]. When their pattern of expression was studied, the former was found to accumulate early and remain throughout ripening, whereas the latter appeared only at the final stage of fruit-color development and was found to be a carotenoid-associated protein [Plant Physiology 91:455-458 (1989)].

Identification of the protein fibrillin in bell peppers as an essential structure component of chromoplast-specific, carotenoid-accumulating lipoprotein structures, termed fibrils, and the isolation of its cDNA and genomic clones were very important steps towards understanding the internal structure of chromoplasts [Plant Cell 6:119-133 (1994)]. Analysis of this gene's expression in bell pepper revealed that both the protein and the transcript accumulate in parallel to fruit ripening. The bell pepper clone, however, did not reveal homologous transcripts in other tissues or plants, *ibid*.

To date, a number of genes from the carotenoid biosynthetic pathway in fruits have been cloned [Plant Mol. Biol. 27:425-428 (1995); Plant Mol. Biol. 27:1153-1162 (1995)]. Of these, however, only one, encoding capsanthin-capsorubin synthase [Plant Cell 7:1027-1038 (1995); Plant J. 6:45-54 (1994); Curr. Genet. 26:524-527 (1994)], shows fruit-chromoplast-specific expression.

Flower pigmentation due to carotenoid accumulation has also been studied. In *Tropaeolum majus* corollas, a 30 kDa protein accumulated in parallel to flower development and appeared to be a major and obligatory component of chromoplast fibrils [Protoplasma 157:128-135 (1990)]. Proteins of 30 and 68 kDa were characterized

as the main proteins of *Viola tricolor* chromoplast globules [Plant Cell Res. 1:111-114 (1982)]. In nasturtium flowers, an immunocomplex band of 32 kDa was revealed with fibrillin antibodies [Plant Cell 6:119-133 (1994)]. With respect to genes of the carotenoid biosynthetic pathway, expression of phytoene synthase (PSY) and phytoene desaturase (PDS) in tomato flowers was shown to peak just before anthesis [Plant Cell 5:379-384 (1993)]. The petals and anthers of mature flowers accumulated the highest levels of these transcripts, as compared with other organs. Nevertheless, expression of both PSY and PDS was found not to be flower-specific.

Young green flower buds of *Cucumis sativus* contain chloroplasts, which are converted to fibrillar chromoplasts as the flower matures. Only chromoplasts are found in the mature yellow corollas [Physiol. Plant 104:321-326 (1994)]. An isolated 35 kDa chromoplast-specific protein (CHRC) from cucumber corollas was shown to be associated with carotenoids. While the above-findings are interesting from the botanical point of view, they do not have a practical utility.

Since carotenoids are so important for both plants and animals it would be of a great advantage to utilize in some way the above findings to achieve and control a higher production or accumulation of carotenoids in plants or cells, or their easy production by bacterial cells.

It is, therefore a primary object of this invention to provide a method for genetic control of production and/or accumulation of high levels of carotenoids in cells of plants, bacteria or other organisms.

SUMMARY

One aspect of the current invention is a method for production, accumulation and sequestration of high amounts of carotenoids in plant, bacteria or other cells by molecular and other type manipulations of carotenoid-associated proteins.

Another aspect of the current invention is a gene of which expression produces a protein which controls and is involved in a production, accumulation and sequestration of carotenoids in plant, bacteria or other cells.

Another aspect of the current invention is a method for molecular cloning of *chrc* gene
5 encoding for the carotenoid-associated protein CHRC from *Cucumis sativus*.

Still another aspect of the current invention is a gene containing domain which is homologous to domains present in a variety of chromoplasts containing plants.

Still another aspect of the current invention is a nucleotide sequence (SEQ ID NO:1) of the *chrc* gene encoding the *Cucumis sativus* protein CHRC.

10 Still another aspect of the current invention is an amino acid sequence (SEQ ID NO:2) comprising 322 amino acid of the CHRC protein of *Cucumis sativus*.

Still yet another aspect of the current invention is a partly sequenced CHRC promoter having a nucleotide sequence (SEQ ID NO:10).

Another aspect of the current invention is a method for high production of carotenoids
15 using bacterial cells having introduced CHRC gene intracellularly together with genes encoding enzymes for carotenoid biosynthesis.

DEFINITIONS

As used herein:

"CHCR" means chromoplast-specific carotenoid-associated protein.

20 "CHRD" means a minor chromoplast-specific protein of about 14 kD isolated from cucumber corolla chromoplasts.

"Anthesis" means the flowering period in flowers and plants.

"Corolla" means collectively the petals and flowers.

"Thylakoid" means a membranous lamella of protein and lipid implant chloroplasts
25 where the photochemical reactions of photosynthesis take place.

"Gibberellins" or "GA" means plant hormones that regulate various aspects of plant growth and development, such as germination, cell growth, stem elongation, flower and fruit development and pigmentation.

"Gibberellin A₃" or "GA₃" means a hormone which up-regulates production of CHRC protein expression.

BRIEF DESCRIPTION OF FIGURES

Figure 1 shows comparative photographs of cucumber flowers petals showing transient expression of the reporter gene GUS using CHRC promoter (Figure 1A) or known 35S CaMV promoter (Figure 1B).

Figure 2 shows a hydropathy plot of the predicted CHRC amino acid sequence determined according to Kyle and Doolittle [*supra.*] using a window size of eight amino acids.

Figure 3 shows *in vitro* transcription/translation of CHRC and import into intact chloroplasts.

Figure 4 is a Northern blot analysis of CHRC expression during cucumber flower development.

Figure 5 is a Northern blot analysis of CHRC mRNA in different cucumber tissues.

Figure 6 is a Northern and Western blot analyses of chromoplast-containing tissues from different plants.

Figure 7 shows kinetics of CHRC mRNA and protein accumulation in response to GA₃.

Figure 8 shows effects of paclobutrazol and ABA on CHRC mRNA level.

Figure 9 shows effect of cyclohexamide on CHRC gene expression.

Figure 10 shows a dose response of CHRC to GA₃.

Figure 11 shows immunodecoration of CHRD in different *Cucumis sativus* organs.

Figure 12 shows changes in the immunologically detectable amounts of CHRD during flower development *in vivo*.

Figure 13 shows identification of CHRD in the carotenoid-protein complex of chromoplasts.

Figure 14 shows effect of GA₃ on CHRD content of *in vitro* cultured corollas.

Figure 15 shows effect of ethylene on CHRC and CHRD levels and effect of etiolation on CHRD levels in corollas.

Figure 16 shows a restriction map of the cloned genomic DNA containing the CHRC's coding and upstream regions

DETAILED DESCRIPTION OF THE INVENTION

This invention concerns proteins and genes involved in carotenoids accumulation, sequestration and production in non-photosynthetic tissues of plants, bacteria or in other cells. The invention discloses a genetic manipulation of certain plants through upregulation of expression resulting in increased production of carotenoid-associated proteins which cause increased accumulation and sequestration of carotenoids in chromoplasts.

Chromoplasts are carotenoid-accumulating plastids found in the corollas and fruits of many higher plants. In most cases, the pigment in these plastids is accumulated with the aid of carotenoid-associated proteins located within unique structures. The invention discovered a method for genetic manipulation of carotenoid accumulation of plastids by providing means for increased production of carotenoid-associated proteins.

I. *chrc* Gene and CHRC Protein Encoded by It

The current invention concerns discovery of the existence of a group of homologous genes coding for chromoplast-specific, carotenoid-associated proteins involved in carotenoid production and accumulation in various plants.

This invention discloses the isolation and characterization of the cDNA of the CHRC gene from *Cucumis sativus* corollas which encodes the chromoplast-specific carotenoid-associated proteins CHRC. The transit peptide cleavage site was determined

and, using a chloroplast uptake system, it was shown that CHRC can be post-translationally targeted to these plastids where they are peripherally associated with thylakoids. Analysis of CHRC transcript level in *Cucumis sativus* revealed its temporal and tissue-specific regulation: the transcript was detected only in corollas, where its level increased in parallel to flower development, peaking just before anthesis.

Immunological analysis of CHRC expression revealed it to be regulated in a temporal and tissue-specific manner. The steady-state levels of CHRC increased in parallel to cucumber flower development and carotenoid accumulation, peaked right before anthesis, dropped to a very low level only 24 hours after anthesis and was undetectable in leaves. Antibodies against CHRC and CHRD also cross-reacted with proteins of approximately 35 kDa in corollas of other representatives of the Cucurbitaceae family, such as squash, melon and watermelon. Results of studies of the effect of hormones on CHRC and carotenoid accumulation shows that gibberellin A₃ (GA₃) is intimately involved in regulation of chromoplast biogenesis in corollas.

CHRC shares significant homology (59%) with the gene coding for fibrillin. Fibrillin is a protein found in *Capsicum annum* red pepper whose function is essentially identical to that of CHRC. A CHRC fragment, including the potential active site of the protein, was used as a probe in Northern blot analyses of floral and fruit tissues from various plants containing chromoplasts of different types. CHRC homologs of similar sizes were revealed in all cases. The existence of a group of homologous genes coding for chromoplast-specific proteins which aid in the sequestration of carotenoids with specific structures seems evident from these findings.

The detection of expression of CHRC counterparts in other fibrillous chromoplast-containing plants, and even in plants with cristallous-and globulous-type chromoplasts such as tomato and orange fruits suggest the existence of a homologous group of genes coding for apoproteins which aid in carotenoid sequestration within chromoplasts. The level of homology within the group, based on the homology between CHRC and

fibrillin, is similar to that between genes coding for enzymes of the carotenoid biosynthetic pathway, such as PSY and PDS.

A. CHRC Gene and Isolation of CHRC cDNA

The present invention additionally concerns the isolation and characterization of the
5 *Cucumis sativus* gene (CHRC) encoding a corolla-chromoplast-specific, carotenoid-associated protein. *Cucumis sativus* gene (CHRC) was isolated and characterized. The gene has been deposited under Access Number: X95593 on February 8, 1996 at the EMBL/Gen Bank/DDBS databases. Nucleotide and deduced amino acid sequences of CHRC cDNA are seen in Table 1.

10 The post-translational targeting of this nuclear-encoded protein to plastids, and the cleavage site of the transit peptide were demonstrated. Based on the expression pattern of this gene in cucumber tissues and of its homologs in chromoplastogenic organs of a number of other plants, the existence of a group of homologous genes coding for chromoplast-specific, carotenoid-associated proteins is proposed.

15 Two degenerate primers, N and R, synthesized according to the N-terminal and internal amino acid microsequences of CHRC, respectively, were used to amplify cucumber corolla (stage 3, 24 hours before anthesis) cDNA. When the resultant PCR product of 443 bp was used as a probe in Northern blot analyses, corolla-tissue-specific signal was revealed. Moreover, when used as a template for PCR with F (an oligonucleotide
20 synthesized according to the internal amino acid sequence) and R primers, an approximately 160 bp product was generated. The 443 bp DNA fragment was cloned and sequenced. The predicted amino acid sequence of the cloned DNA fragment exhibited a 100% match to the three available microsequences of CHRC.

To isolate cDNA encoding the entire CHRC, a corolla cDNA library was constructed
25 and screened with the cloned DNA fragment. The largest insert contained in one of the positive clones was fully sequenced. This cDNA, termed CHRC, contained a region

with a sequence identical to that yielded by PCR. The CHRC cDNA is seen in SEQ ID NO:1 and in Table 1. Table 1 shows nucleotide sequence (SEQ ID NO:1) of CHRC gene and predicted amino acid sequence (SEQ ID NO:2) of its expressed carotenoid-associated CHRC protein. Nucleotide sequence consists of 74 bp 5'-untranslated region, a 966 bp open reading frame, a stop codon and a 293 bp 3'-untranslated region including a 27 bp poly(A) tail. The N-terminal and two internal peptide microsequences are underlined. The sequence of the PCR-generated 443 bp product is in bold face. The arrowhead indicates the cleavage site of the transit peptide and the translation terminal codon is marked with an asterisk. The CHRC precursor protein, based on the derived sequence of 322 amino acids, had a predicted molecular mass of 35.2 kDa and consisted of two parts: a 58 amino-acid-long transit peptide and a mature protein (264 amino acids) with a predicted molecular mass of 29.3 kDa. Based on its mobility on an SDS-PAGE, the molecular mass of the mature CHRC was estimated at 35 kDa. Furthermore, expression in *Escherichia coli* yielded an approximately 41 kDa protein that cross-reacted with CHRC antisera (not shown). The cleavage point of the precursor protein (between amino acids R and A) (Figure 1a) was determined based on the N-terminal microsequence of the mature CHRC.

Table 1

Nucleotide and Predicted Amino Acid Sequences

	AGTAAATCCC AGTCCTTCAG TTTGTGCTTT TGTGTGTTTT GTTCTCTGA TTTACGGAAT	60
	TTGGAAATAA TTCTATGGCG TTTGTTTCTA AATTCAATCA ACTTCCGTGC AAGACTCTCG	120
5	M A F V S Q F N Q L P C K T L A	16
	CACTCAATCC ACCACAACCT CAATTGACTT CTAAGCCTTC GGTTTTCCCC ATCGCTTCGA	180
	L N P P Q P Q L T S K P S V F P I A S I	36
	TTGGGGCTAC CGCCAGAGCC GCGGCGGGGA AGTCACTGAT CTCAGTTAGG CCTGCGTTCA	240
	G A T A R A A A G K S L I S V R P A F K	56
10	AGGTCCGTGC GGTGTTAAAC GATGACGAGT GGGGGGAGGA TAAGGATGAG AAGTATGGAG	300
	<u>V R A V L N D D E W G E D K D E K Y G D</u>	76
	ATGATTCTGC TGTGGCGGTA GCTGAAAAGG AGGAGGAAAA GCCTCTGGAG CCATCCGAGA	360
	<u>D S S V A V A E K E E E K P L E P S E I</u>	96
	TTTATAAACT GAAGAAGGCG TTGGTGGACT CGTTTTACTT GACCGATCGT GGATTACGAG	420
15	Y K L K K A L V D S F Y G T D R G L R V	116
	TGTCCAGAGA TACTAGGGCG GAGATTGTCG AGCTGATTAC GCAACTGGAA TCGAAGAACC	480
	S R D T R A E I V E L I T Q L E S K N P	136
	CAACCCCTGC TCCTACTGAG GCCCTGACTC TGCTCAACGG CAAGTGGATT CTAGCGTACA	540
	T P A P T E A L T L L N G K W I L A Y T	156
20	CAACTTTCGC GGGTCTGTTC CCGTTGTTGT CTAGGAATTT GCCATTGGTC AAAGTGGAGG	600
	T F A G L F P L L S R N L P L V K V E <u>E</u>	176
	AAATTTACA GACAATTGAT TCAGAGAAVV TCACCGTCCA AAATCTGTG CAGTTTTCCG	680
	<u>I S Q T I D S E N L T V Q N S V Q F S G</u>	196
	GTCCTCTAGC CACCACTTCC ATTACTACCA ATGCAAAGTT TGAAGTTCGA AGTCCCCTGC	720
25	P L A T T S I T T N A K F E V R S P L R	216
	GTGTACATAT CAAATTCGAA GAAGGTGTCA TTGGAAGTCC CCAGCTGACG GATTGATAG	780
	<u>V H I K F E E G V I G T P Q L T D S I V</u>	236
	TGATACCAGA TAATGTGGAC TTTCTTGGGC AGAAGATTGA CTTTACACCA TTCAATGGTA	840
	I P D N V D F L G Q K I D F T P F N G I	256
30	TCATATCTTC CCTTCAAGAC ACTGCTTCAA ATGTAGCCAA GACGATTTG AGTCAACCAC	900
	I S S L Q D T A S N V A K T I S S Q P P	276
	CAATCAAGTT CTCAATCTCA AACACGAGGG TAGAGTCTTG GTTGCTAACT ACTTATCTTG	960
	I K F S I S N T R V E S W L L T T Y L D	296
	ATGAAGATCT TCGAATTCA CGAGGAGATG GTGGTAGCGT GTTCGTACTC CTCAAGGAAG	1020
35	E D L R I S R G D G G S V F V L L K E G	316
	GCAGTTCTTT CTTGTCTCTC TAAACACCCT TACTCTTCTC ACTATAAAGG GTTCATAGGA	1080

S S F L S L 322
 AACTGAATTA TTATTCAAGG ATGTTTTTAA ACGTGTTGTA GTTCTTATC AAATAGTGAA 1140
 TGATATTGCC TTCTGTTCAA AGGGCCAGCT TCAATTAGCT TCATCTTCTT TAAATCACT 1200
 AGTTACTTGA ATTTCTGTTG AGAAAATAAA CATTGTTTAT ATTTTACCCA TACTGTACCA 1260
 5 AAAGCCAAAA GTTAAACCAA AACGTGTGAA AAGCTTGGAA GGGCTTGAC polyA 1309

SEQ ID NO:1 of 1309 nucleotides, seen in Table 1, is a cDNA sequence of the *chrc* gene. Fragments and variants thereof are domains comprising nucleotides 309-379, 663-705 or 803-831. These fragments and their variants are intended to be within the scope of the invention.

SEQ ID NO:2 of 322 amino acids, seen in Table 1, is an amino acid sequence of CHRC protein. Fragments and variants thereof are domains comprising amino acids 59-82, 177-191 and 224-233. These fragments and their variants are intended to be within the scope of this invention.

15 Figure 2 shows a hydropathy plot of the predicted amino acid sequence determined according the Kyte and Doolittle [J. Mol. Biol. 157:105-132 (1982)] using a window size of eight amino acids. Increased hydrophobicity is indicated by positive values. The hydropathy plot showed hydrophobic regions in the C-terminal portion of the transit peptide and in the middle and C-terminal portions of the mature protein. The most hydrophilic region was situated in the N-terminal portion of the mature protein. The predicted pI of the mature CHRC was 4.9, whereas that of the CHRC transit peptide was 12.3.

Table 2

Comparison of CHRC and Fibrillin

25	CHRC	MAFVSQFNQL PCKTLALNPP QPQLTSKPSVFP . IASIGATARAAAGKSLI
	Fibrillin	MASISLNLQI PCKTLQITSQ YSKISLPLT SPNFPSKTEL HRSISIKEFT
	CHRC	SVRPAFKVRAVLNDDEWGEDKDEKYGDDSSVAVAEKEEEKPLEPSEIYKL
	Fibrillin	NPKPKFTAQATNYDKE . . DEWGPELEQINPGGVAVVEEPPKEPSEMEKL

	CHRC	KKALVDSFYGTDRGLRVSRD <u>TRAEIVELITQLESKNPTPAPTEALTLLNG</u>	
	Fibrillin	KKQLTDSFYGTNRGLSASSET <u>TRAEIVELITQLESKNPTPAPTEALSLLNG</u>	
	CHRC	<i>KWILAYTTFAGLFPLLSR</i> .NLPLVKVEEISQTIDSENLTVQNSVQFSGPL	
	Fibrillin	KWILAYTSFSGLFPLLARGNLLPVRVEEISQTIDAETLTVQNSVVFAGPL	
5	CHRC	ATTSITTNAKFEVRSPLRVHIKFEEGVIGTPQLTDSIVIPDNVDLFGQKI	
	Fibrillin	STTSISTNAKFEVRSPKRLQINFEEGIIGTPQLTDSIELPENVEFLGQKI	
	CHRC	DFTPFNGISSLQDTASNVAKTISSQPPIKFSISNTRVESWLLTTYLDED	
	Fibrillin	DLSPFKGLITSVQDTATSVAKSISSQPPIKFPISNSYAQSWLLTTYLDAE	
	CHRC	LRISRGDGGSVFVLLKEGSSFLSL	322 amino acids
10	Fibrillin	LRISRGDAGSIFVLIKEGSPLLKP	322 amino acids

The cucumber CHRC cDNA clone isolated and characterized in the present invention shared no significant homology with previously published sequences available in GeneBank, aside from that of fibrillin. The two proteins of similar molecular mass shared a number of common features: a positively charged transit peptide, acidic pI of the mature protein, a similar three-dimensional structure based on hydropathy profiles, a lack of cysteine residues, tandem glutamic/aspartic acid residues, identical 7 and 25 amino acid domains in transit and mature peptides, respectively, a probably helical transmembrane region which is 90% identical, and a cell adhesion motif. Table 2 compares amino acid sequences of CHRC and fibrillin, a carotenoid-associated protein from red peppers. As seen in Table 2, CHRC and fibrillin from pepper fruits shared 59% homology at the DNA level, and 64% identity/74% similarity at the amino acid level. Comparison of CHRC and fibrillin amino acid sequences, seen in Table 2 shows the highly conserved regions in the transit peptide (8-15) and in the mature protein (120-144) are underlined. Amino acids in italicized bold face indicate the probably helical transmembrane region (147-164). The arrow indicates the cleavage site of the transit peptide. The potential cell adhesion motif is double-underlined. The longest region in CHRC exhibiting 100% identity with the corresponding region in fibrillin spanned residues 120-144. Despite their low level of homology (32% identity/48% similarity), transit peptides of CHRC and fibrillin shared a common domain of seven

amino acids. Similar to fibrillin, the mature CHRC did not contain any cysteine residues, and had several tandem aspartic and/or glutamic acid residues at positions 63-65, 68-69, 71-72, 86-88, 176-177 and 222-223. A highly probably helical transmembrane region was detected for amino acids 147-164 in both CHRC and fibrillin. The two sequences also shared the potential cell adhesion motif RGD as described in Trends Biol. Sci. 16:246-260 (1991) at position 303. This high level of similarity between CHRC and fibrillin reflects their similar structural role in fibrillous-type chromoplasts, irrespective of organ or plant type.

B. *In vitro* Transcription/Translation and Targeting to Chloroplasts

In vitro transcription/translation of CHRC and import into intact chloroplasts is seen in Figure 3. In Figure 3A, the CHRC cDNA was transcribed and translated *in vitro* and the radio-labeled product (RP) was analyzed by SDS-PAGE followed by fluorography. Immunological blotting of the CHRC translation product (IP) and of Cab7 (Cab7) as a control was performed using antibodies against CHRC. Figure 3B shows SDS-PAGE and fluorography of stromal (lanes 1, 3 and 5) and thylakoid (lanes 2, 4 and 6) subfractions obtained from thermolysin-treated chloroplasts following import of radio-labeled CHRC (lanes 1 and 2), SSU (lanes 3 and 4) and Cab7 (lanes 5 and 6) precursors. Radio-labeled CHRC precursor is shown in lane P. Molecular mass markers are indicated on the left.

In vitro transcription/translation of the CHRC cDNA clone yield a 41 kDa radio-labeled product that cross-reacted with CHRC-specific antibodies as seen in Figure 3A. When the radio-labeled CHRC precursor was incubated with intact chloroplasts, followed by treatment with thermolysin, only the processed CHRC, having a mobility consistent with that of authentic mature CHRC, was revealed. Following chloroplast fractionation, as seen in Figure 3B, the processed CHRC was found to be associated with thylakoids and was not observed in the stromal fraction.

Parallel uptake experiments with chloroplast-specific radio-labeled chlorophyll a/b binding protein (Cab7) and the small subunit (SSU) of Rubisco revealed the following results. The processed Cab7 was found in the thylakoids, whereas SSU was observed in the stromal fraction. To characterize the association between the imported CHRC and the thylakoids, the isolated membranes were treated with either NaOH or thermolysin for 30 minutes. Following either of these treatments, the protein did not remain associated with the membranes and was only revealed in the NaOH-wash fraction (data not shown), suggesting that when present in chloroplasts, it is peripherally associated with thylakoid membranes.

10 C. *Expression of CHRC mRNA*

The expression pattern of CHRC at the RNA level was regulated in a temporal and tissue-specific manner. A very similar pattern of expression has been revealed for CHRC at the protein level. Using an *in vitro* flower bud culture system that mimics *in vivo* flower development, CHRC mRNA levels in corollas were shown to be specifically up-regulated by gibberellic acid. The patterns of CHRC up-regulation by GA₃ and down-regulation by abscisic acid and ethylene were observed to be essentially identical at both protein and RNA levels.

Figures 4-6 show temporal and tissue-specific regulation of CHRC transcript in corollas.

20 Figure 4 is Northern blot analysis of CHRC expression during cucumber flower development. In Figure 4, total RNA extracted from cucumber flower corollas at stages 1-5 (lanes 1-5) was probed with radio-labeled CHRC cDNA. The same RNA blot was rehybridized with 18S ribosomal RNA probe (rRNA). Stage 1 corollas were green and contained chloroplasts, whereas fully developed corollas at anthesis (stage 4) were yellow and contained only chromoplasts. In parallel to flower development, the level of CHRC RNA, approximately 1.3 kb, increased up to stage 3, that is 24 hours before

anthesis. It could be barely detected at anthesis and was undetectable in stage 5 corollas, that is 24 hours after anthesis.

Figure 5 shows results of Northern blot analysis of CHRC mRNA in different cucumber tissues. In Figure 5, total RNA extracted from cucumber corollas (C), fruits
5 (F), stems (S), leaves (L) and roots (R) was probed with radiolabeled CHRC cDNA. The same RNA blot was rehybridized with 18S ribosomal RNA probe (rRNA).

As seen in Figure 5, the analysis of CHRC expression in various cucumber tissues revealed a high level of CHRC transcript in the RNA from corollas, whereas transcript could not be detected in the other tissues analyzed, even under low-stringency
10 hybridization conditions.

To study whether CHRC has counterparts in chromoplast-containing tissues of other plants, Northern blot analysis was performed with RNA extracted from fruits and corollas of various plant species.

Figure 6 shows results of Northern and Western blot analyses of chromoplast-
15 containing tissues from different plants. In Figure 6, total RNA (a) and total protein (b) were extracted from cucumber (1), melon (2) and watermelon (3) corollas, pepper fruits (4), *Helenium* (5) and tomato (6) corollas, tomato fruits (7) and orange peels (8). The RNA blot was probed with a CHRC cDNA fragment (480-765). The same RNA blot was rehybridized with 18S ribosomal RNA probe (rRNA). Northern blot analysis is
20 shown in Figure 6A. Using CHRC as a probe, a strong hybridization signal was revealed in the corollas of melon (*Cucumis melo* L.) and watermelon (*Citrullus vulgaris* Schrad.), both of which contain fibrillar chromoplasts. The transcript size in these plants, which belong to the Cucurbitaceae family along with the cucumber, was identical to that of the cucumber CHRC RNA. Much weaker signals of a slightly
25 different size were observed in read bell pepper fruits (*Capsicum annum* L.) and in yellow corollas of *Helenium autumnale* L. No hybridization signal was revealed with RNA from orange peels (*Citrus sinensis* L.), or from tomato corollas or fruits

(*Lycopersicon esculentum* L.) (data not shown). On the other hand, when a CHRC fragment (480-765) which is highly homologous to fibrillin (85% similarity) was used as a probe, the hybridization signal was also seen in tomato corollas and red fruits, and in orange peels. This fragment includes the potentially active sites of CHRC, comprising surface loops and a trans-membrane helix, but does not include regions of low homology such as that coding for transit peptide, and the 5' and 3' untranslated regions.

Western blot analysis, as seen in Figure 6B, was performed using antibodies against CHRC protein. Using a sensitive ECL detection system immuno-complex bands with a mobility of approximately 35 kDa was revealed.

Based on the above findings, genes for carotenoid synthesis and accumulation were shown to be strongly regulated at the transcriptional level.

D. *GA₃* Involvement in Up-Regulation of CHRC Synthesis

Gibberellins (GAs) are plant hormones that regulate various aspects of plant growth and development, such as germination, cell growth, stem elongation, flower and fruit development, and pigmentation.

The involvement of GAs in various aspects of cucumber (*Cucumis sativus* L.) floral organ development is well documented. The involvement of a specific hormone *GA₃* in chromoplast biogenesis in corollas was characterized. Two chromoplast-specific carotenoid-associated proteins (CHRC and CHRD) were identified and shown to be specifically up-regulated by *GA₃*. The effect of antagonists and inhibitors of *GA₃*, such as abscisic acid and paclobutrazol, and an inhibitor of protein synthesis, such as cycloheximide, were studied and their effect on *GA₃* upregulation of CHRC synthesis was determined.

An *in vitro* flower bud culture system, previously shown to mimic *in vivo* flower development was used to study the effect of *GA₃* on CHRC expression. Isolation and

characterization of a single-copy gene coding for CHRC allowed determination of GA regulatory function of carotenoid-associated proteins.

Results of the studies involving the effect of GA₃ is seen in Figures 7 and 8.

Figure 7 shows kinetics of CHRC mRNA and protein accumulation in response to GA₃. Young flower buds were cultured *in vitro* in the presence (GA) or the absence (C) of 100μM GA₃ for up to 48 hours. Northern and Western blot analyses of corollas, cultured for the indicated periods of time, were performed. The Northern blots (25 g total RNA/lane) were hybridized with ³²P-labeled DNA inserts from CHRC (CHRC), MEL6 (Psy), and 18s rDNA (18S). Western blot analysis (bottom panel of A) was performed using antibodies against CHRC protein (25 g total protein/lane). The results of the CHRC Northern blot analyses are also shown graphically relative to the mRNA level of the untreated corollas at zero time (0) (arbitrary value of 1).

As seen in Figure 7, CHRC mRNA level was very rapidly affected by exogenous GA₃ (Figure 7A); after 20 minutes of treatment, it was approximately twice as high in treated versus control corollas. With longer incubation periods, the level of CHRC mRNA in GA₃-treated corollas increased further, to approximately 5-or 6-fold that of untreated control corollas. A closer examination of early time points revealed a detectable increase in CHRC mRNA level within 10-20 minutes in response to GA₃ (data not shown). At the protein level, the effect of GA₃ on CHRC was slower; after 2 hours of treatment, approximately 2.5 times more CHRC per unit of protein had accumulated in treated versus control corollas (Figure 7A). No change in the total protein content of corollas was detected within 6 hours of treatment. To determine whether GA₃ also affects the expression of genes encoding enzymes from the carotenoid biosynthesis pathway, the expression of Psy, the first committed gene of that pathway, was studied. Psy mRNA levels were rather stable during the first 45 hours of corollas development and were not affected by GA₃ treatment.

To further characterize the involvement of GAs in CHRC expression, the effect of paclobutrazol, an inhibitor of GA synthesis, on CHRC mRNA levels was analyzed. Results are seen in Figure 8.

Figure 8 shows effects of paclobutrazol and ABA on CHRC mRNA level. Flower buds were cultured in the presence of 100 μ M GA₃ (GA), 100 μ g/ml paclobutrazol following 2 hours of pretreatment with 100 μ g/ml paclobutrazol (P), 100 μ M/ml paclobutrazol + 100 μ M GA₃ following 2 hours of pretreatment with 100 μ g/ml paclobutrazol (P/GA), 100 μ M ABA (ABA), or no phytohormones (C). Total RNA was extracted from corollas after 2 hours of treatment. Northern blot analyses were performed and probed as described in the legend to Fig. 7.

As seen in Figure 8, the addition of paclobutrazol to the *in vitro* bud culture system led to a 4-fold decrease in CHRC mRNA levels relative to control untreated corollas. Inclusion of exogenous GA₃ in addition to paclobutrazol not only prevented the down-regulation, it up-regulated CHRC transcript accumulation to the level of GA₃-treated corollas.

ABA antagonizes GA in many developmental processes and has been shown to have an inhibitory effect on CHRC protein accumulation. To obtain additional support for the role of GA₃ in the regulation of CHRC expression, the effect of ABA on CHRC transcript accumulation was analyzed. When 100 μ M ABA was added to the *in vitro* bud culture system, the CHRC mRNA level was down-regulated 2.5 times as compared with control corollas. The inhibitory effect of ABA on CHRC transcript accumulation was concentration-dependent. Application of 10 μ M ABA only slightly down-regulated CHRC expression. Neither ABA nor paclobutrazol markedly affected Psy mRNA levels.

To study the effect of protein synthesis inhibition on the up-regulation of CHRC by GA₃, the protein synthesis inhibitor cycloheximide (CHX) was used. For this purpose,

cucumber flower buds were cultured with or without CHX in the presence of GA₃. Results are seen in Figure 9.

Figure 9 shows effect of cycloheximide on CHRC gene expression. Total RNA and protein were extracted from cucumber corollas of flower buds cultured for 6 hours in the presence of 100 μ M GA₃ (GA), 50 μ M CHX following 2 hours of pretreatment with 50 μ M CHX (CHX/GA), or no phytohormones (C). Northern (CHRC, Psy, and 18S) and Western (bottom panel) blot analyses were performed as described above.

As can be seen from Figure 9, 50 μ M CHX did not prevent the up-regulation of CHRC mRNA by GA₃, whereas it successfully abolished the increase in CHRC protein levels in GA₃-treated buds. CHX alone did not affect CHRC transcript accumulation, in contrast to its up-regulating effect on the early response GAmYb gene in barley aleurone cells. Psy mRNA levels in corollas were also unaffected by CHX treatment.

The sensitivity of CHRC expression to GA₃ was also assessed. For that purpose, a dose response curve ranging from 1×10^{-8} to 1×10^{-4} M GA₃ was obtained after exposing grown flower buds *in vitro* to the GA₃ for 2 hours. Results are seen in Figure 10.

In Figure 10, flower buds were cultured for 2 hours without (0) or with various concentrations of GA₃. Total RNA was isolated from corollas, and a Northern blot was probed as above. The results of the CHRC Northern blot analyses are also shown graphically relative to the mRNA level of control corollas cultured without GA₃ (arbitrary value of 1).

As seen in Figure 10, CHRC was strongly up-regulated at 10^{-5} - 10^{-4} M, whereas concentrations as low as 10^{-7} M were sufficient to markedly elevate basal CHRC mRNA levels. A similar response curve has been described for the primary GA-responsive gene, pmyb92, in petunia.

In the studies described above, the upregulation of CHRC synthesis in response to GA₃ acid was observable already within 20 minutes. Such response was insensitive to protein synthesis inhibitor cycloheximide. Absciscic acid and paclobutrazol strongly

down-regulated CHRC mRNA levels. CHRC mRNA accumulation in response to gibberellic acid displayed a dose-dependent increase up to 10^{-4} M gibberellic acid. The up-regulation could be detected with as little as 10^{-7} M gibberellic acid.

chrc gene is the first structural gene identified to date whose expression is regulated by GA₃ in a primary fashion. The rapid response of CHRC to GA₃ followed by increased carotenoid accumulation and sequestration shows that such carotenoid accumulation is genetically regulated by the *chrc* gene which encodes CHRC proteins. A crucial role for GAs during flower development, chromoplastogenesis and carotenoid accumulation in *C. sativus* was discovered.

- 10 Control of carotenogenesis by GA₃ seems to be executed via regulation of downstream carotenoid biosynthesis enzymes and/or carotenoid sequestration. CHRC's rapid up-regulation in response to GA₃ is crucial for enhanced carotenoid accumulation in the chromoplast.

The method for production of carotenoids involves accumulation, sequestration or high production of the carotenoids in the plants chromoplasts or in bacterial or other cells by providing these cells with genetic apparatus for increased expression of CHRC protein which, as shown above is involved in greater accumulation, sequestration or carotenoid production. In practice, the plants or bacteria are transfected with *chrc* gene encoding CHRC protein and the expression of this protein is enhanced with GA₃ in combination with CHRC promoter in plants and with any suitable promoter in bacteria or other cells or tissue. In this way, the plants or bacteria accumulate large amounts of carotenoids which are harvested and purified as necessary for their intended use.

II. CHRD - A Minor Chromoplast-Specific Protein

- 25 In addition to CHRC protein, the invention also concerns discovery of chromoplast protein D (CHRD). Compared to CHRC protein, the CHRD protein of about 14 kD is minor in abundance. When the polypeptide compositions of chromoplasts, chloroplasts, and corollas at different developmental stages were determined and compared, the

CHRD was present in chromoplasts, undetectable in chloroplasts, and accumulated in corollas in parallel with flower development as determined by Coomassie brilliant blue staining. Chromoplast protein D (CHRD) was isolated from cucumber corolla chromoplasts. Immunological characterization revealed that the protein is chromoplast-specific and that its steady-state level in corollas increases in parallel to flower development. The protein was not detected in cucumber leaves or fruits. Immunological analysis of corollas and fruits from a variety of other plants also did not reveal cross-reactivity with the CHRD protein antisera.

Similarly to the studies described for CHRC protein, GA₃ rapidly enhanced, whereas paclobutrazol down-regulated, the steady-state level of CHRD. Ethylene also down-regulated the protein's steady-state level. These results show that hormonal control of chromoplastogenesis is tightly regulated at the tissue/organ level. Results of the above studies are shown in Figures 11-15.

Figure 11 shows immunodecoration of CHRD in different *C. sativus* organs. Total protein extracted from leaf (L), fruit (F), corolla (P) (50 µg per lane), and chromoplasts (C) (10 µg of protein) were electrophoresed on a 14% SDS-polyacrylamide gel and analyzed by western blotting using antibodies against CHRD and alkaline phosphatase anti-rabbit 1gG. CB, Coomassie brilliant blue-stained total proteins (25 µg) from chromoplasts.

Based on densitometry analyses, CHRD constitutes about 1% of the total chromoplast proteins resolved by SDS-PAGE. The protein was isolated and used to prepare antiserum, and the resultant antiserum cross-reacted with isolated CHRD and did not cross-react with isolated CHRC or chloroplasts. Preimmune serum did not reveal any signal when used in a western blot analysis of corollas, chromoplasts, or isolated CHRD. The affinity-purified antibodies against CHRD were found to be tissue-specific: they did not cross-react with the total protein fraction of cucumber leaves or fruits, whereas a strong signal was obtained with corollas and isolated chromoplasts.

During flower development the immunologically detectable level of CHRD increased in corollas up to anthesis and then decreased to a low level, as seen in Figure 12.

Figure 12 shows changes in the immunologically detectable amounts of CHRD during flower development *in vivo*. Total protein (50 µg per lane) extracted from leaf (lane 1),
5 corollas at stages 1 through 5 (lanes 2-6, respectively), and chromoplasts (10 µg, lane 7) was electrophoresed on a 14% SDS-polyacrylamide gel and analyzed by western blotting.

To examine the possible relationship between CHRD and chromoplast pigments, the plastids were solubilized with various detergent combinations and fractionated on a
10 non-denaturing gel. Results are seen in Figure 13.

Figure 13 shows identification of CHRD in the carotenoid-protein complex of chromoplasts. Chromoplast membranes isolated from corollas at anthesis were solubilized with 2% n-octyl α-D-glucopyranoside, 1% n-nonyl α-D-glucopyranoside, 1% n-decyl α-D-glucopyranoside, and 0.3% SDS (w/v) and fractionated on a
15 nondenaturing Deriphatpolyacrylamide gel for 30 minutes at 100 V. The gel was photographed without fixing or staining (A). The entire lane was excised from the gel and cut into three pieces (lanes I-III). Proteins were extracted from these gel slices, re-electrophoresed on a fully denaturing 14% SDS-polyacrylamide gel, and analyzed by western blotting using CHRC (B) and CHRD (C) antibodies, FP, Free pigment zone.

20 A distinct, slow-migrating, yellow band was revealed under the following solubilization conditions: 2, 1, 1, and 0.3%; 1, 1, 2, and 0.3%; or 1, 2, 1, and (w/v) octyl glucoside, nonyl glucoside, decyl glucoside, and SDS, respectively. Western blot analysis of the polypeptides extracted from this distinct band and resolved by fully denaturing SDS-PAGE revealed the presence of CHRD and CHRC (Fig. 3). Coomassie brilliant blue
25 staining of the SDS gels revealed CHRC to be the major polypeptide associated with these yellow bands.

To test for CHRD antigenic counterparts in chromoplastogenic organs of other plants, CHRD antibodies were cross-reacted with fruits and petals of a variety of different plants. Unlike CHRC, which is abundant in several other flowers, CHRD antiserum did not cross-react with corollas of melon, watermelon, daffodil, or rose, or with fruits of pepper or tomato, or with carrot.

Effects of developmental and environmental factors on CHRD accumulation were further studied.

Previous studies have shown the usefulness of the *in vitro* bud culture system, which fully resembles flower development with respect to carotenoid and CHRC accumulation, for studies of the involvement of growth regulators in chromoplast biogenesis. This system was, therefore, used to study the developmental regulation of CHRD expression in corollas. Inclusion of GA₃ in the culture medium resulted in enhanced accumulation of CHRD, as seen in Figure 14.

Figure 14 shows effect of GA₃ on the CHRD content of *in vitro* cultured corollas.

Figure 14A shows young flower buds cultured for 72 hours in the presence of GA₃ (G), ABA (A), or paclobutrazol (P) or without phytohormones (C). CHRD levels in corollas were analyzed by western blotting (10 µg of total protein per lane) using antibodies against CHRD and horseradish peroxidase anti-rabbit IgG in an enhanced chemiluminescence detection system. Figure 14B is a Western blot analysis of corollas (50 µg of total protein per lane) cultured for the indicated periods with (+) or without (-) GA₃. The blot was decorated with antibodies against CHRD and alkaline phosphatase anti-rabbit IgG.

When paclobutrazol, an inhibitor of GA₃ synthesis, was added to the *in vitro* bud culture system, the CHRD level per unit protein was down-regulated 4.8 ± 0.2 times as compared with control untreated corollas. A lower level of CHRD was also detected in corollas treated with ABA, which is known to be antagonistic to GA₃ in several systems (2.5 ± 0.3 times lower than that of control untreated corollas per unit protein),

seen in Figure 14A. The up-regulation of CHRD by GA₃ was very rapid, and after only 2 hours its level was markedly higher in treated versus untreated buds. No difference was noted in fresh weight or total protein level between treated and control corollas for up to 24 hours in culture.

5 The effect of ethylene, a growth regulator associated with fruit ripening and flower senescence on the accumulation of chromoplast-specific proteins is shown in Figure 15. Figure 15 shows the effect of ethylene or CHRC and CHRD levels and of etiolation on CHRD levels in corollas. In Figure 15A, antibodies against CHRD or CHRC were used in a western blot analysis of CHRD and CHRC levels, respectively, in corollas cultured
10 for 72 hours in the presence (E) or absence (C) of ethylene (50 µg of total protein per lane). In Figure 15B, flowers were enclosed in aluminum foil in the greenhouse for 3 days and CHRD levels in etiolated (D) and control, nonetiolated (L) corollas were analyzed by western blotting (50 µg of total protein per lane).

As seen in Figure 15B, the level of CHRD per unit protein was down-regulated
15 following treatment with ethylene. Moreover, the level of CHRC in ethylene-treated corollas was also lower than that in controls.

Carotenoids, in contrast to chlorophyll, accumulate in the dark. To monitor the effect of light, CHRD levels in *in vivo* etiolated corollas were analyzed. Figure 15B shows the CHRD level per unit protein in corollas of etiolated buds to be enhanced as compared
20 with that in control corollas of light-grown buds. Effects of both ethylene and etiolation on CHRD levels normalized per corolla were even more pronounced, since the total protein content of the treated corollas was, respectively, 50% lower and 30% higher than that of control, untreated corollas.

Compared to CHRC, CHRD is only a minor protein, however, its function corresponds
25 to CHRC function in carotenoids accumulation in chromoplasts.

III. The CHRC Promoter

The invention additionally concerns a discovery of a new CHRC promoter useful for directing of CHRC gene expression.

The new promoter was partly sequenced. The sequenced portion of the CHRC promoter has a sequence SEQ ID NO:10.

Briefly, a cucumber subgenomic library was prepared by digesting cucumber genomic DNA with Hind III and a clone containing the coding sequence for CHRC and its approximate 1.4 kb of the upstream region was isolated and sequenced. An approximately 2.1 kb DNA fragment 5' to the sequenced upstream region was also cloned. Cloning was performed using EcoRI-digested genomic DNA. Approximately 3.5 kb of the CHRC upstream region has been cloned as seen on the restriction map seen in Figure 16. Figure 16 shows a restriction map of the genomic DNA containing CHRC coding and upstream regions.

Figure 16 is a reconstructed restriction map of genomic DNA fragment that contains upstream and coding regions of CHRC. 3'EcoRI site is approximately 150 nucleotides upstream to ATG. The sequence of the promoter region and the beginning of the transcribed region was obtained from cloned genomic HindIII fragment.

The sequenced upstream region was found to possess strong promoter activity and was found to be very efficient in the expression of a foreign gene GUS. The promoter containing CHRC upstream region was about 70% as efficient as the 35S CaMV promoter in cucumber petals and about 60% as efficient in leaves, fruits and stems. The CHRC promoter's efficiency in another representative of the cucurbit family, namely in melon, was similar to the efficiency found in cucumber.

Because CHRC gene expression is strongly regulated by a number of environmental and developmental signals, the cis elements within the promoter are very important and are, therefore, useful for generating and directing inducible and/or tissue specific gene expression in genes other than in *Cucurbitacea*.

UTILITY

The invention provides for high production and accumulation of carotenoids which are highly important to both animals and plants. Carotenoids produced according to the invention are used as essential dietary components added to the food for human consumption, as active ingredients of antioxidants and vitamins which possess anticancer activity and protect the human subjects from heart and age related diseases. Commercially, they are useful as food products colorants or as additives to pharmaceutical drugs. In agriculture, they are useful for enhancement of flower, fruit or plants colors. In photosynthetically active organisms, carotenoids are essential to the proper functioning of the light-harvesting apparatus and they determine color of fruits and flowers.

The current invention discloses new gene for expression of proteins effecting accumulation and sequestration of carotenoids in plant chromoplasts. Derived from the new genes is a new promoter and a nucleotide sequence thereof which allows expression of any other foreign gene.

The invention is useful for production of plants producing large amounts of carotenoids. Carotenoids are important for medicinal purposes, as antioxidants, vitamin A precursors, food colorants, for production and variability of flower colors and as protective anti-cancer agents.

Production of carotenoids using expression of the discovered genes allows production of large quantities of carotenoids in a very practical and inexpensive way. Due to the presence of the carotenoid-binding domain within CHRC or CHRD, these proteins are potentially useful for efficient accumulation of carotenoids within any cell, not only those of plant origin.

The invention also enables production of carotenoids using the bacterial expression systems where CHRC or CHRD is introduced into bacteria in combination with enzymes for carotenoid biosynthesis, to increase the levels of accumulating carotenoids.

EXAMPLE 1 - Plant material

This example describes plant material used for the current studies.

Cucumber (*Cucumis sativus* L.) plants (cultivar-Shimanon) obtained from Zeraim Gedera, Israel were grown under standard greenhouse conditions. Stages of flower development were as described in Plant Physiol. 104:321326 (1994): stages 1, 2, and 3 occurred 120, 72, and 24 hours before anthesis, respectively, stage 4 at anthesis, and stage 5, 24 hours after anthesis. all tissues were used immediately after collection or frozen in liquid nitrogen and stored at -70°C.

EXAMPLE 2 - Plant Material and *In Vitro* Flower Bud Culture

10 This example describes plant material and conditions for *in vitro* flower bud culture.

C. sativus L. plants (cultivar Shimahon, obtained from Zeraim Gadera, Israel) were grown under standard greenhouse conditions. *In vitro* culture of flower buds was performed at 23°C, under constant light from cool white fluorescent lamps with a photosynthetic photon flux density of 80 μ mol/m² g, as described previously. Briefly, buds at developmental stage 1 (~8 mm in length, 120 hours before anthesis) were collected and rinsed several times with sterile water. Buds were then placed for 24 hours on a perforated Parafilm (American National Can, Greenwich, CT) covering a Petri dish filled with double-distilled sterile water, such that only the bases of the buds were in contact with the liquid. Following equilibration, buds were transferred to a fresh Petri dish (zero time for the experiments) and treated with GA₃, ABA, paclobutrazol, or CHX, as specified in the figure legends.

EXAMPLE 3 - RNA Isolation and Northern Blot Analysis

This example describes conditions used for RNA isolation and Northern blot analysis.

Total RNA from corollas of cucumber flower buds was isolated as described previously. RNA (15 and 25 µg) was fractionated through a 1.2% formaldehyde gel and transferred to a Hybond-N⁻ filter (Amersham Corp.). A random priming kit (Boehringer Mannheim) was used to radioactively labeled DNA probes. The blots were
5 hybridized with ³²P-labeled cucumber CHRC cDNA 916) and reprobred with melon phytoene synthase (PSY) cDNA (MEL5), provided by D. Grierson of the Nottingham University, UK. The hybridization for analysis of CHRC expression was carried out in 0.263 M Na₂HPO₄, 7% SDS, 1 µM EDTA, 1% BSA for 16 hours at 60°C, and the washes were performed in 2xSSC/0.1% SDS at 50°C followed by 2xSSC/0.1% SDS at
10 55°C, for 20 minutes each. Hybridization with the MEL5 probe was carried out at 55°C using the same procedure. Following the hybridization, the blots were washed in 5xSSC/0.1% SDS at 45°C for 20 minutes followed by 5xSSC/0.1% SDS at 50°C and 2xSSC/0.1% SDS at 50°C for 20 minutes each. Autoradiograms were quantified by scanning suitably exposed films in a densitometer (Molecular Dynamics, Sunnyvale,
15 CA). The amount of RNA loaded onto the gels was standardized by optical measurement, by quantitation of the ethidium bromide fluorescence of cytoplasmic rRNA, and by the level of hybridization with a DNA fragment coding for cytoplasmic 18S RNA.

20 **EXAMPLE 4 - SDS-PAGE, Protein Digestion, Amino Acid Sequencing and Western Blotting**

This example describes conditions used for SDS-PAGE, protein digestion, amino acid sequencing and Western blotting.

Chromoplast isolation and SDS-PAGE were performed as described in Plant Physiol. 102:491-496 (1993). The CHRC protein bands excised from SDS gels stained with
25 Coomassie Blue were digested with *Staphylococcus aureus* V8 protease (Sigma), by placing gel slices containing the protein into the sample wells of a second SDS gel and

then overlaying with the protease according to J. Biol. Chem. 252:1102-1106 (1977). Following electrophoresis, peptides were electrotransferred on to a polyvinylidene difluoride (PVDF) membrane obtained from Bio-Rad according to J. Biol. Chem. 262:10035-10038 (1987), stained with Coomassie Blue, and sequenced directly.

5 Automated Edman sequencing was performed using an AB1 475A gas phase microsequencer (Applied Biosystems). The Western blot analyses were performed with an ECL Western blotting detection system (Amersham), using affinity-purified polyclonal antibodies against CHRC, Plant Physiol. 104:321-326 (1993) and horse-radish peroxidase anti-rabbit IgG (Sigma) as a second antibody.

10 **EXAMPLE 5 - PCR Amplification of cDNA Probe**

This example describes PCR amplification procedure of cDNA probe.

Total RNA (40 µg) from corollas of stage 3 cucumber flower buds was isolated according to EMBO J. 7:1257-1263 (1988) and used for first-strand cDNA synthesis described in Molecular Cloning: A Laboratory Manual, Cold Spring Harbor, N.Y.,
15 Cold Spring Harbor Laboratory Press (1993). PCR amplification was performed using degenerate primers synthesized according to the amino acid microsequences of CHRC. Two forward primers were synthesized: 5'GGAATTCGAIAAITA(C/T)GGIGAIGA (SEQ ID NO:4), termed N, encoding the amino acid sequence EKYGD (SEQ ID NO:5) and having an EcoRI restriction site at its 5'-terminus, and 5'-
20 GA(G/A)AATTCCCA(G/A)AC(C/T)AT(T/C)GAT (SEQ ID NO:6), termed F, encoding the amino acid sequence EISQTID (SEQ ID NO:7). The reverse primer used was 5'CA(A/G)(C/T)TGTGG(T/A)GTTCC(T/G)ATTA (SEQ ID NO:8), termed R, reflecting the complementary strand of DNA encoding the amino acid sequence IGTPQL (SEQ ID NO:9).

The first primer was synthesized according to the N-terminal amino acid microsequence of undigested CHRC, and the latter two were synthesized according to internal CHRC microsequences (Table 1).

The following reaction mixture was used for PCR: 50 mM KCl, 10 mM Tris-Cl pH 8.3, 1.0 mM MgCl₂, 60 μM of each dNTP, 0.4 μM of each primer and 1.5 units of Taq polymerase (Advanced Biotechnologies). The samples were heated to 94°C for 2 minutes, followed by annealing at 50°C for 2 minutes and elongation at 72°C for 2 minutes. The amplification was continued for 30 cycles at 94°C for 30 seconds, 55°C for 1 minute, and 72°C for 1 minute. After the last amplification cycle, the samples were incubated at 72°C for 10 minutes. Following electrophoresis on a 2.0% agarose gel and subsequent purification (Jetsorb, Genomed Inc.), a 443 bp PCR product was cloned into pBluescript KS (Stratagene).

EXAMPLE 6 - Construction and Screening of cDNA Library

This example describes conditions for construction and screening of cDNA library.

Poly(A)⁺ RNA was purified from stage 3 flower corolla total RNA using PolyAtract mRNA isolation system 1 (Promega), and 5 μg were used to construct a cDNA library in a Uni-ZapTM XR vector using a ZAP-cDNA[®] synthesis kit and Gigapack II packaging extracts (Stratagene). Approximately 10⁵ phages were screened with the radioactively labeled 443 bp PCR fragment and DNA was isolated from 15 positive clones. Hybridization was carried out for 16 hours at 65°C and the filters were washed twice with 2xSSC/0.1% SDS at 65°C (1xSSC = 0.15 M NaCl/0.015 M trisodium citrate pH 7.0).

EXAMPLE 7 - CHRC DNA Sequencing and Analysis

This example describes CHRC gene DNA sequencing and analysis.

Nucleotide sequences were determined by Dye Terminator Sequencing, using a Taq Dye Deoxy Terminator Cycle Sequencing Kit (Applied Biosystems). To avoid the sequencing errors that can occur with long DNA fragments (greater than 500 bp), the cDNA clones were sequenced using restriction fragments, and external (Bluescript) and internal (cDNA) specific primers in two directions each. DNA and protein sequences were analyzed using the GCG Wisconsin Package. Transmembrane protein predictions were based on PHDhtm (Neural Network System) according to J. Mol. Biol. 232:584-599 (1993) and TMpred Biol. Chem. Hoppe Seyer, 374:166 (1993) programs.

EXAMPLE 8 - *In Vitro* Transcription Translation and Import Assay

This example describes transcription, translation and import assay.

The CHRC cDNA clone was subcloned into pSP73, which was then used as a template in a coupled transcription/translation system (Promega) containing SP6 RNA polymerase and wheat-germ extract. The reaction was performed in the presence of [³H]-Leu (Amersham), to yield a radio-labeled precursor protein. Isolation of intact chloroplasts from pea seedlings, import reactions and detection of imported proteins were all performed as recently described in Plant Mol. Biol. 29:53-61 (1995). Fractionation of stroma and thylakoids, and alkali and protease treatments of thylakoids were performed as described in Plant Physiol. 99:247-255 (1992). pGEM4 Cab7 and pSP65 SSU were used to prepare Cab7 and SSU radio-labeled precursors, respectively, Plant Physiol. 102:35-42 (1993) and Plant Mol. Biol. 29:53-61 (1995). These were used as controls in the chloroplast uptake experiments. Post-import detection of proteins was performed by SDS-PAGE and fluorography.

EXAMPLE 9 - Northern Blot Analysis

This example describes conditions used for Northern blot analysis.

Total RNA (10 µg) was fractionated through a 1.2% formaldehyde gel and transferred to a Hybond-N⁺ filter (Amersham). Membranes were probed with DNA fragments radio-actively labeled using a random priming kit (Boehringer Mannheim). The hybridization for analysis of CHRC expression during corolla development, presented in Figure 10, was carried out in 0.263 M Na₂HPO₄, 7% SDS, 1 mM EDTA, 1% bovine serum albumin (BSA) for 16 hours at 60°C and the washes were performed in 2xSSC/0.1% SDS at 50°C for 20 minutes followed by 2xSSC/0.1% SDS at 55°C. Hybridization for other total RNA blots was carried out at 55°C using the same hybridization procedure. Following the hybridization, the blots were washed in 5xSSC/0.1% SDS at 45°C for 20 minutes followed by 5xSSC/0.1% SDS at 50°C and 2xSSC/0.1% SDS at 50°C for 20 minutes each. The amount of RNA loaded on to the gels was standardized by optical measurement, by quantitation of the ethidium bromide fluorescence of cytoplasmic rRNA and by the level of hybridization with a cytoplasmic rRNA probe coding for cytoplasmic 18S RNA, Plant Physiol. 104:321-326 (1993).

EXAMPLE 10 - Chromoplast Specific Protein

This example describes preparation and testing of chromoplast specific protein of 14 kD (CHRD).

CHRD protein was isolated from *Cucumis sativus* as a minor component, immunologically characterised and analyzed in terms of the regulation of its expression by developmental signals using methods and conditions described above for CHRC. CHRD was found in chromoplasts, was undetectable in chloroplasts and accumulated in corollas in parallel to flower development. During flower development, the immunologically detectable levels of CHRD increased in corollas up to anthesis and then dropped to a low level. As with CHRC, the level of CHRD was found to be very

rapidly upregulated by GA₃; after only 2 hours of culture, its levels were markedly higher in GA₃ treated compared to untreated buds. No difference was noted in fresh weight or total protein level between treated and control corollas for up to 24 hours in culture. When treated with abscisic acid (ABA), known GA₃ antagonist, or
5 paclobutrazol, an inhibitor of GA₃ synthesis, was added to the in vitro bud-culture, CHRD levels were downregulated. Levels of both proteins, CHRC and CHRD were very strongly downregulated following treatment with ethylene, a growth regulator which promotes chloroplast-chromoplast conversion in fruits. The involvement of CHRD in carotenoid production, accumulation or sequestration in plants is further
10 confirmed by the findings that the CHRD levels in corollas of etiolated buds was enhanced in darkness as compared to that in control corollas of light-grown buds. Carotenoids are known to accumulate in dark.

EXAMPLE 11 - The CHRC Promoter

This example describes a sequencing of a new CHRC promoter for expression of
15 CHRC and other foreign genes.

A cucumber subgenomic library was prepared by digesting genomic DNA with Hind III. A clone containing the coding sequence for CHRC and its approximate 1.4 kb of the upstream region was isolated and sequenced. In addition, approximately 2.1 kb DNA fragment 5' to the sequenced upstream region was also cloned. Cloning was
20 performed using EcoRI-digested genomic DNA. As a result, approximately 3.5 kb of the CHRC upstream region has been cloned as seen on the restriction map (Figure 16). The cloned promoter or a portion thereof has a sequence identified as SEQ ID NO:10.

The sequenced upstream region possessed strong promoter activity. In cucumber petals, the CHRC upstream region was about 70% as efficient as the 35S CaMV promoter. In
25 leaves, fruits and stems, the CHRC promoter was about 60% as efficient as 35S CaMV. Promoter's efficiency in melon was similar to that observed in cucumber.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: YISSUM RESEARCH DEVELOPMENT COMPANY
OF THE HEBREW UNIVERSITY OF JERUSALEM

(ii) TITLE OF INVENTION: CAROTENOID ASSOCIATED PROTEINS
USEFUL FOR HIGH CAROTENOID
ACCUMULATION AND PRODUCTION IN
PLANTS AND OTHER ORGANISMS

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: A. E. Mulford
(B) STREET: P. O. Box 544
(C) CITY: Jerusalem
(D) STATE:
(E) COUNTRY: ISRAEL
(F) ZIP: 91004

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette - 3.5 inch. 1.44 Kb storage
(B) COMPUTER: PC
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: Microsoft Word 6.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/032421
(B) FILING DATE: December 5, 1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Michal Hackmey
(B) REGISTRATION NUMBER:
(C) REFERENCE/DOCKET NUMBER:

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (972-2) 6231122
(B) TELEFAX: (972-2) 6246542

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cucumis sativum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AGTAAATCCC	AGTCCTTCAG	TTTGTGCTTT	TGTGTGTTTT	GTTTCTCTGA	TTTACGGAAT	60
TTGGAATATA	TTCTATGGCG	TTTGTTTCTA	AATTCAATCA	ACTTCCGTGC	AAGACTCTCG	120
CACTCAATCC	ACCACAACCT	CAATTGACTT	CTAAGCCTTC	GGTTTCCCC	ATCGCTTCGA	180
TTGGGGGTAC	CGCCAGAGCC	GCGGCGGGGA	AGTCACTGAT	CTCAGTTAGG	CCTGCGTTCA	240
AGGTCCGTGC	GGTGTAAAC	GATGACGAGT	GGGGGGAGGA	TAAGGATGAG	AAGTATGGAG	300
ATGATTCTGC	TGTGGCGGTA	GCTGAAAAGG	AGGAGGAAAA	GCCTCTGGAG	CCATCCGAGA	360
TTTATAAACT	GAAGAAGGCG	TTGGTGGACT	CGTTTACTT	GACCGATCGT	GGATTACGAG	420
TGTCCAGAGA	TACTAGGGCG	GAGATTGTCT	AGCTGATTAC	GCAACTGGAA	TCCAAGAACC	480
CAACCCCTGC	TCCTACTGAG	GCCCTGACTC	TGCTCAACGG	CAAGTGGATT	CTAGCGTACA	540
CAACTTTTCG	GGGTCTGTTT	CCGTTGTTGT	CTAGGAATT	GCCATTGGTC	AAAGTGGAGG	600
AAATTTTACA	GACAATTGAT	TCAGAGAAVV	TCACCGTCCA	AAACTCTGTC	CAGTTTTCCG	660
GTCCTCTAGC	CACCACTTCC	ATTACTACCA	ATGCAAAGTT	TGAAGTTCCA	AGTCCCCTGC	720
GTGTACATAT	CAAATTCGAA	GAAGGTGTCA	TTGGAAGTCC	CCAGCTGACG	GATTCGATAG	780
TGATACCAGA	TAATGTGGAC	TTTCTTGGGC	AGAAGATTGA	CTTTACACCA	TTCAATGGTA	840
TCATATCTTC	CCTTCAAGAC	ACTGCTTCAA	ATGTAGCCAA	GACGATTTCT	AGTCAACCAC	900
CAATCAAGTT	CTCAATCTCA	AACACGAGGG	TAGAGTCTTG	GTTGCTAACT	ACTTATCTTG	960
ATCAAGATCT	TCGAATTTCA	CGAGGAGATG	GTGGTAGCGT	GTTCTGACTC	CTCAAGGAAG	1020
GCAGTCTCTT	CTTGTCTCTC	TAAACACCTT	TACTCTTCTC	ACTATAAAGG	GTTTATAGGA	1080
AACTGAATTA	TTATTCAAGG	ATGTTTTTAA	ACGTGTTGTA	GTTTCTTATC	AAATAGTGAA	1140
TGATATTGCC	TTCTGTTCAT	AGGGCCAGCT	TCAATTAGCT	TCATCTTCTT	TTAAATCACT	1200
AGTTACTTGA	ATTTCTGTTG	AGAAAATAAA	CATTGTTTAT	ATTTTACCCA	TACTGTACCA	1260
AAAGCCAAAA	GTAAACCAA	AACGTGTGAA	AAGCTTGGAA	GGGCTTGAC		1309

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Cucumis sativus*

(ix) FEATURE

- (A) NAME/KEY: CHCR protein
- (B) IDENTIFICATION METHOD: deduced

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

met ala phe val ser gln phe asn gln leu pro cys lys thr leu

1	5	10	15
ala leu asn pro pro	gln pro gln leu thr	ser lys pro ser val	
20	25	30	
phe pro ile ala ser	ile gly ala thr ala	arg ala ala ala gly	
35	40	45	
lys ser leu ile ser	val arg pro ala phe	lys val arg ala val	
50	55	60	
leu asn asp asp glu	trp gly glu asp lys	asp glu lys tyr gly	
65	70	75	
asp asp ser ser val	ala val ala glu lys	glu glu glu lys pro	
80	85	90	
leu glu pro ser glu	ile tyr lys leu lys	lys ala leu val asp	
95	100	105	
ser phe tyr gly thr	asp arg gly leu arg	val ser arg asp thr	
110	115	120	
arg ala glu ile val	glu leu ile thr gln	leu glu ser lys asn	
125	130	135	
pro thr pro ala pro	thr glu ala leu thr	leu leu asn gly lys	
140	145	150	
trp ile leu ala tyr	thr thr phe ala gly	leu phe pro leu leu	
155	160	165	
ser arg asn leu pro	leu val lys val glu	glu ile ser gln thr	
170	175	180	
ile asp ser glu asn	leu thr val gln asn	ser val gln phe ser	
185	190	195	
gly pro leu ala thr	thr ser ile thr thr	asn ala lys phe glu	
200	205	210	
val arg ser pro leu	arg val his ile lys	phe glu glu gly val	
215	220	225	
ile gly thr pro gln	leu thr asp ser ile	val ile pro asp asn	
230	235	240	
val asp phe leu gly	gln lys ile asp phe	thr pro phe asn gly	
245	250	255	
ile ile ser ser leu	gln asp thr ala ser	asn val ala lys thr	
260	265	270	
ile ser ser gln pro	pro ile lys phe ser	ile ser asn thr arg	
275	280	285	
val glu ser trp leu	leu thr thr tyr leu	asp glu asp leu arg	
290	295	300	
ile ser arg gly asp	gly gly ser val phe	val leu leu lys glu	
305	310	315	
gly ser ser phe leu	ser leu		
320			

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

37

(A) ORGANISM: *Capsicum annum* L.

(ix) FEATURE

(A) NAME/KEY: fibrillin

(B) IDENTIFICATION METHOD: deduced

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

met	ala	ser	ile	ser	ser	leu	asn	gln	ile	pro	cys	lys	thr	leu	
1				5					10					15	
gln	ile	thr	ser	gln	tyr	ser	lys	ile	ser	ser	leu	pro	leu	thr	
				20					25					30	
ser	pro	asn	phe	pro	ser	lys	thr	glu	leu	his	arg	ser	ile	ser	
				35					40					45	
ile	lys	glu	phe	thr	asn	pro	lys	pro	lys	phe	thr	ala	gln	ala	
				50					55					60	
thr	asn	tyr	asp	lys	glu	asp	glu	trp	gly	pro	glu	leu	glu	gln	
				65					70					75	
ile	asn	pro	gly	gly	val	ala	val	val	glu	glu	glu	pro	pro	lys	
				80					85					90	
glu	pro	ser	glu	met	glu	lys	leu	lys	lys	gln	leu	thr	asp	ser	
				95					100					105	
phe	tyr	gly	thr	asn	arg	gly	leu	ser	ala	ser	ser	glu	thr	arg	
				110					115					120	
ala	glu	ile	val	glu	leu	ile	thr	gln	leu	glu	ser	lys	asn	pro	
				125					130					135	
thr	pro	ala	pro	thr	glu	ala	leu	ser	leu	leu	asn	gly	lys	trp	
				140					145					150	
ile	leu	ala	tyr	thr	ser	phe	ser	gly	leu	phe	pro	leu	leu	ala	
				155					160					165	
arg	gly	asn	leu	leu	pro	val	arg	val	glu	glu	ile	ser	gln	thr	
				170					175					180	
ile	asp	ala	glu	thr	leu	thr	val	gln	asn	ser	val	val	phe	ala	
				185					190					195	
gly	pro	leu	ser	thr	thr	ser	ile	ser	thr	asn	ala	lys	phe	glu	
				200					205					210	
val	arg	ser	pro	lys	arg	leu	gln	ile	asn	phe	glu	glu	gly	ile	
				215					220					225	
ile	gly	thr	pro	gln	leu	thr	asp	ser	ile	glu	leu	pro	glu	asn	
				230					235					240	
val	glu	phe	leu	gly	gln	lys	ile	asp	leu	ser	pro	phe	lys	gly	
				245					250					255	
leu	ile	thr	ser	val	gln	asp	thr	ala	thr	ser	val	ala	lys	ser	
				260					265					270	
ile	ser	ser	gln	pro	pro	ile	lys	phe	pro	ile	ser	asn	ser	tyr	
				275					280					285	
ala	gln	ser	trp	leu	leu	thr	thr	tyr	leu	asp	ala	glu	leu	arg	
				290					295					300	
ile	ser	arg	gly	asp	ala	gly	ser	ile	phe	val	leu	ile	lys	glu	
				305					310					315	
gly	ser	pro	leu	leu	lys	pro									
				320											

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic oligonucleotide

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GGAATTCGAI AAITAC/TGGIG AIGA

24

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Cucumis sativum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

glu lys tyr gly asp
5

(2) INFORMATION FOR SEQ ID NO: 6

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic oligonucleotide

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

GA(G/A)AATTCCC A(G/A)AC(C/T)AT(T/C)GA T

21

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

39

- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Cucumis sativum*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
glu ile ser gln thr ile asp
5

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: synthetic oligonucleotide
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
CA(A/G)(C/T)TGTGG(T/A) GTTCC(T/G)ATTA

20

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Cucumis sativum*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
ile gly thr pro gln leu
5

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: synthetic nucleotide
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AAGCTTTACA AATTAGGGTT ACTTTATTCA TTTTCATCCA TTCTCTTTAT TGTAAATTT	60
TGTACATTTA TTCAATAATA TTATATGTTT ATTACAAATT CTCACCTTCT TATTCATACC	120
TATTCACCTCA AGCCTTTACC ATCTTCCTTT TCTATTTCAA TACTATTTCT ACTTCATTTT	180
TCACGTTTTT AACATCTTTC TTTATTTCTT GTCCACTTCG TTTAGGGATG CCTAATGTCC	240
CAAATTTTCAT CTCTCGTAGT AACACAAAAC CAATGTAATG CTACTTCTCT CTACATTTTT	300
AATACAAATA AAGTGAAACA AAATATCTAT AAATAAACAA ATATATATAT TTTGTTAGAC	360
GCTGTCTCAA CCCATCAATT AAAAAATTTT GTTATATTTT TACTTTACCT ACTAAATTTG	420
TTTCTCATAT TTACCTTTTA ACCCCCACAA AAAAAATTA TAAAAAGAA AGAAAAAGC	480
TAAACCCTAT TTAAATAGCT AACTATAAGA TCTTAAAT ATCCTCATCA GTGTATAGTT	540
TAATTGGTTA TTAACCTTATA ACATTATATA TCTATGACAT ATACTCTCTC CTAGCTATTT	600
CTCACATTTT TTAACCTAAG AAAATAGTCA TAACATAGTC TAAATTCAA ACATCCACAT	660
GCTCTAATTT GATTAAACAA AAGTTAGAAA TATTTATTTA AATAAAAAAG ACTAATAAAT	720
ATATAAAATG AATGTTTATA CGCAGACCCA TTTAGAGATG AGTATGCTTT CACATGCTGA	780
GATTATTTTC AAAACTAAGG TTGTAGCAAT ATTAAATCAA TAAATTTATT ATAAATAACA	840
AAATTAACCT GCTCGTGTTT GCTGTATATG GGAGGCTACA AAATAAATTA AACTAAAGAT	900
GATTATGTTT TAGACATTTT TTCTATCTGT ATTAGTTTAT ACATATTAAT TCAGGAGCTG	960
CACAACCCAA TTCTATTTTC GTTCCTTGGT GGCTGGGTTT CTCACAAGGT TCAATAGTCA	1020
ATATTAGGTT TTATTGGACT TTTAATAGTA TCAAACAAAT CTATGTGTGA ACTTAAAAAT	1080
TGTATTAAAT ATTTAGGGTA ACCTGTTGCC GTTTTATAGAA TAATGTTTCT TCTTAATACA	1140
CGAAAGCGTA TTGTGTATTC ATTCATTTGG CGCCTCACAT GCTTCGGTTG GCTCGCTTTA	1200
GTCTCTGCCT TCTTTGTATA TTGTACTCCC CCTCTTCCTA TGCCACGTGT TCTGAGCTTA	1260
ACAAGCCACG TTGCGTGCCA TTGCCAACA AGTCATTTTA ACTTCACAAG GTCCGATTTG	1320
ACCTCCAAAA CAACGACAAG TTTCGAACA GTCCGAAGA TCAAGGCTAT AATCGTCTTT	1380
TTGAATTCTA TTTCTCTTTA TTTAATAGTC CCTCTCGTGT GATAGTTTTT AAAAGATTTT	1440
TAAAACGTAG CTGCTGTTTA AGTAAATCCC AGTCCTTCAG TTTGT	1485

CLAIMS

1. A DNA sequence identified as SEQ ID NO:1 or fragment or variant thereof.
2. The sequence of claim 2 wherein the fragment is a domain comprising nucleotides 309-379, 663-705, 803-831 or a variant thereof.
3. An amino acid sequence identified as SEQ ID NO:2 or a fragment or variant thereof.
4. The amino acid sequence of Claim 3 wherein the fragment comprises amino acids 59-82, 177-191, 224-233 or a variant thereof.
5. The protein of Claim 3 having highly conserved regions 8-15 in the transit peptide and 120-144 in the mature peptide.
6. A protein which is a product of the DNA sequence SEQ ID NO:1 or a fragment or variant thereof useful for increased accumulation levels or carotenoids.
7. *C. sativus chrc* gene and its homologs coding for a chromoplast-specific protein.
8. A method for increased accumulation and sequestration of carotenoids comprising increased expression for CHRC protein.
9. The method of claim 8 additionally comprising enhancing of carotenoid accumulation or sequestration by addition of plant hormone GA₃.
10. A promoter identified as a SEQ ID NO:10 or a fragment thereof.

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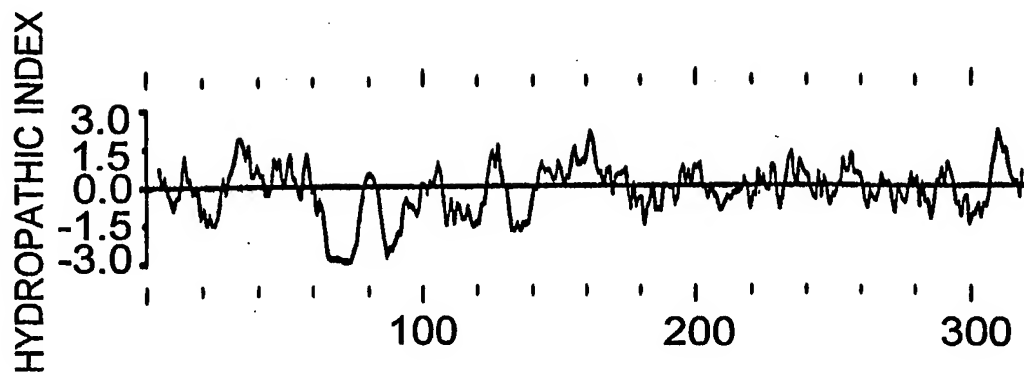
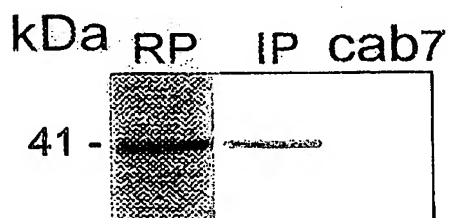
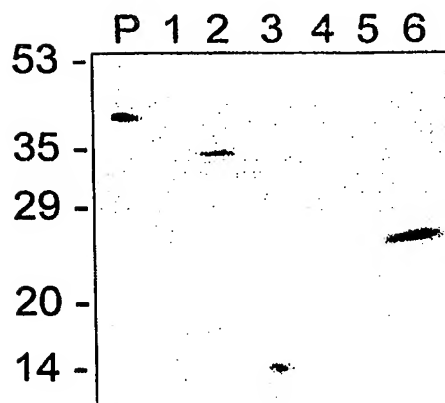
Figure 1A

2/11



Figure 1B

3/11

**Figure 2****Figure 3A****Figure 3B**

4/11

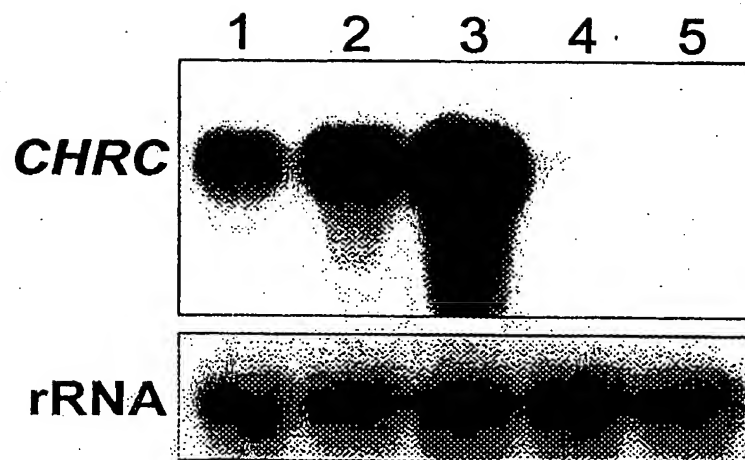


Figure 4

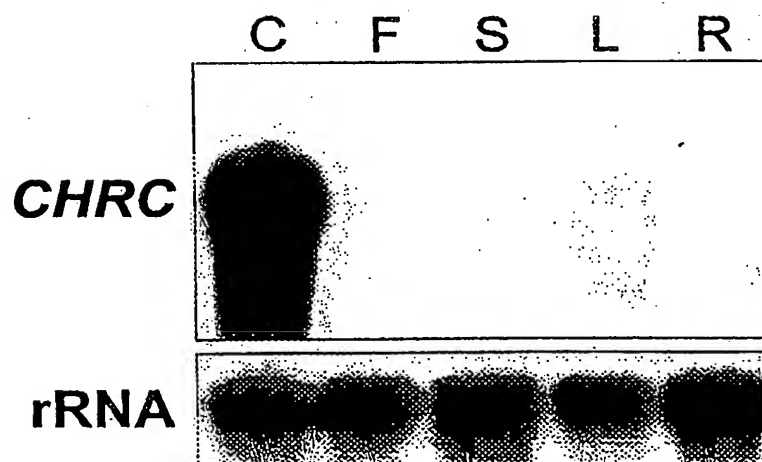


Figure 5

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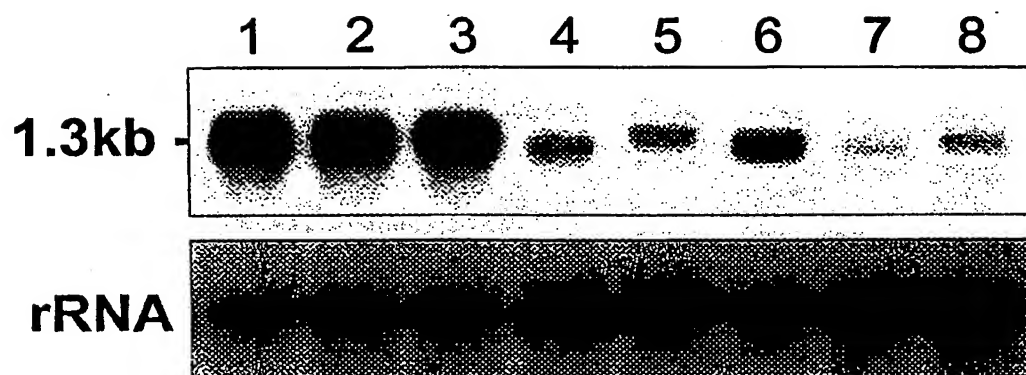


Figure 6A

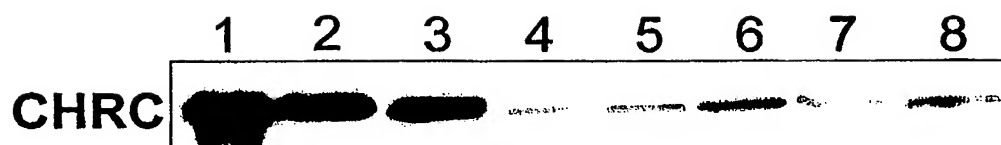


Figure 6B

6/11

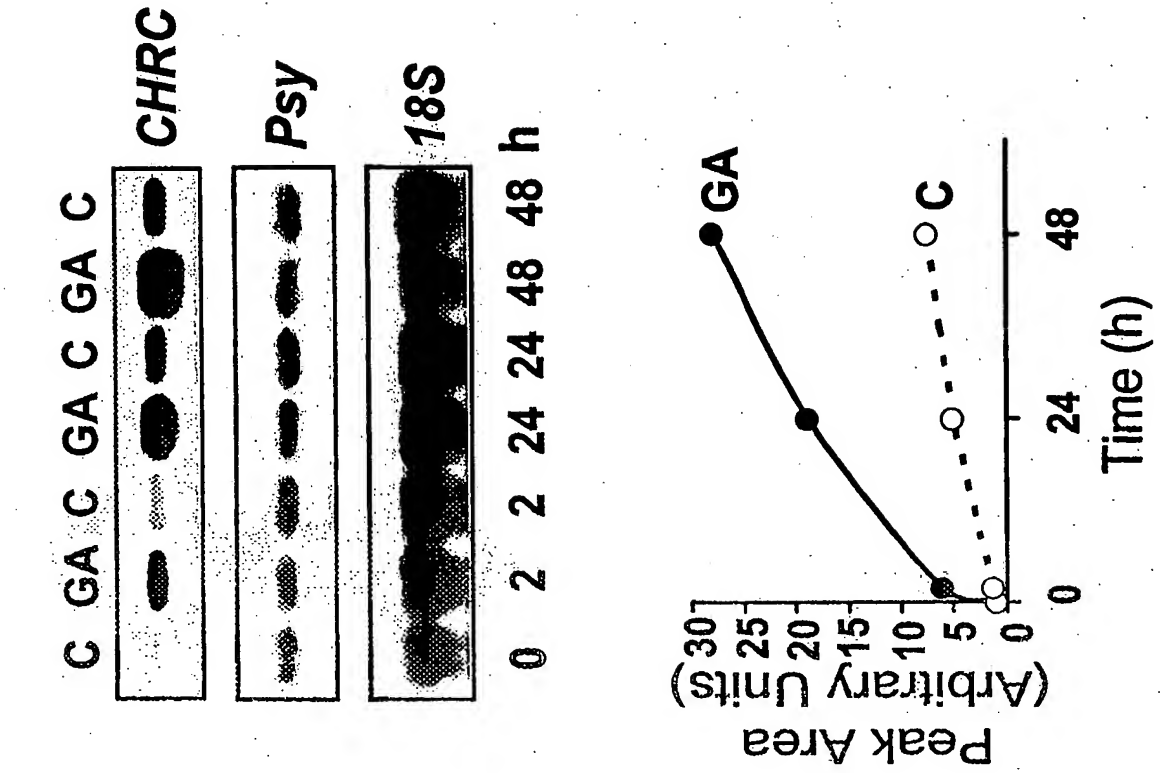


Figure 7A

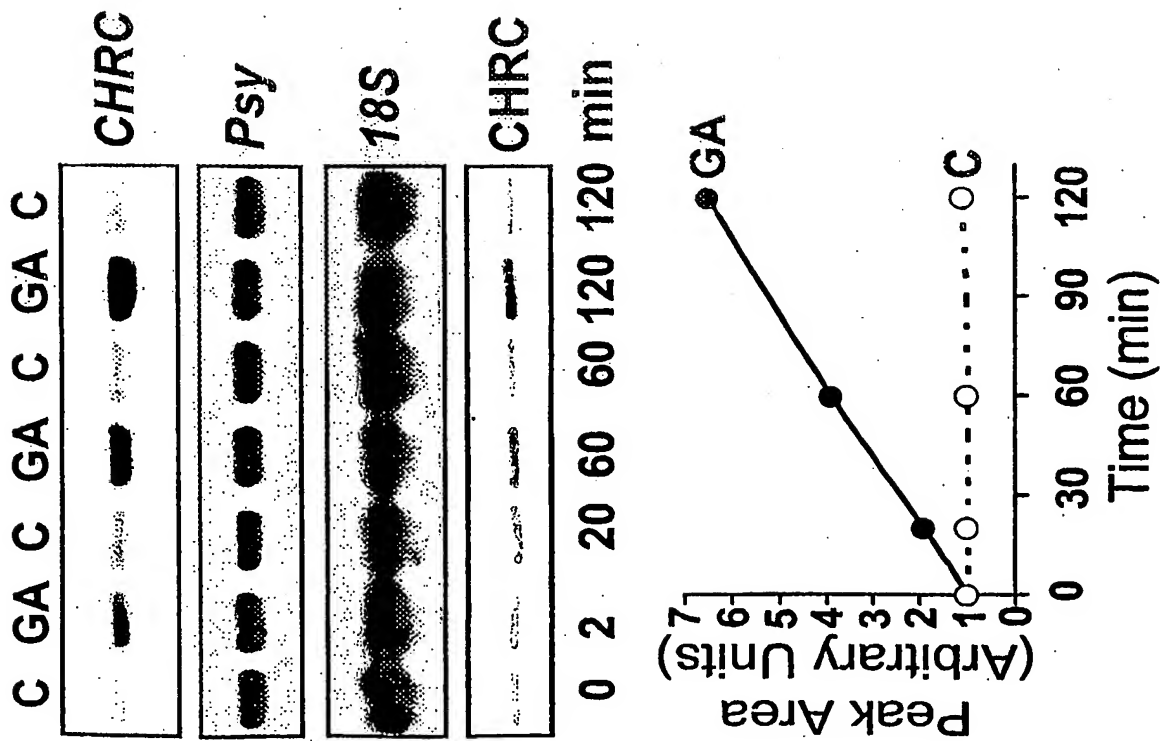


Figure 7B

7/11

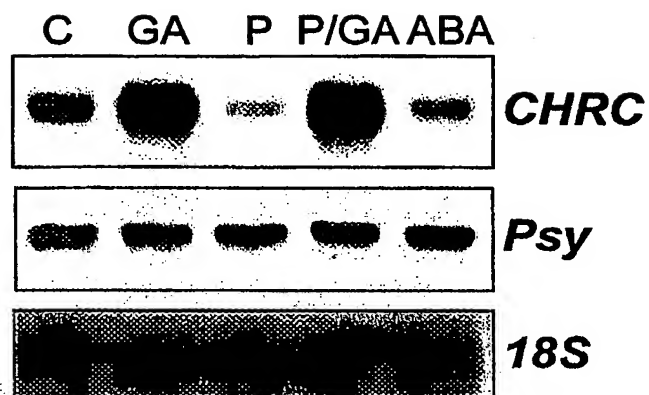


Figure 8

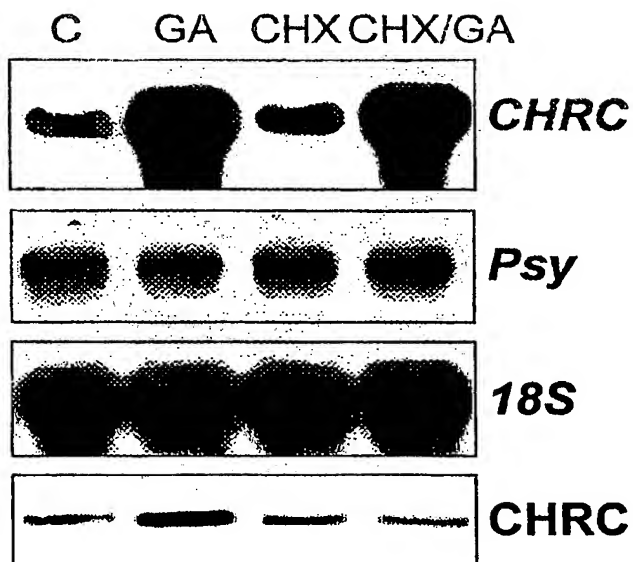


Figure 9

8/11

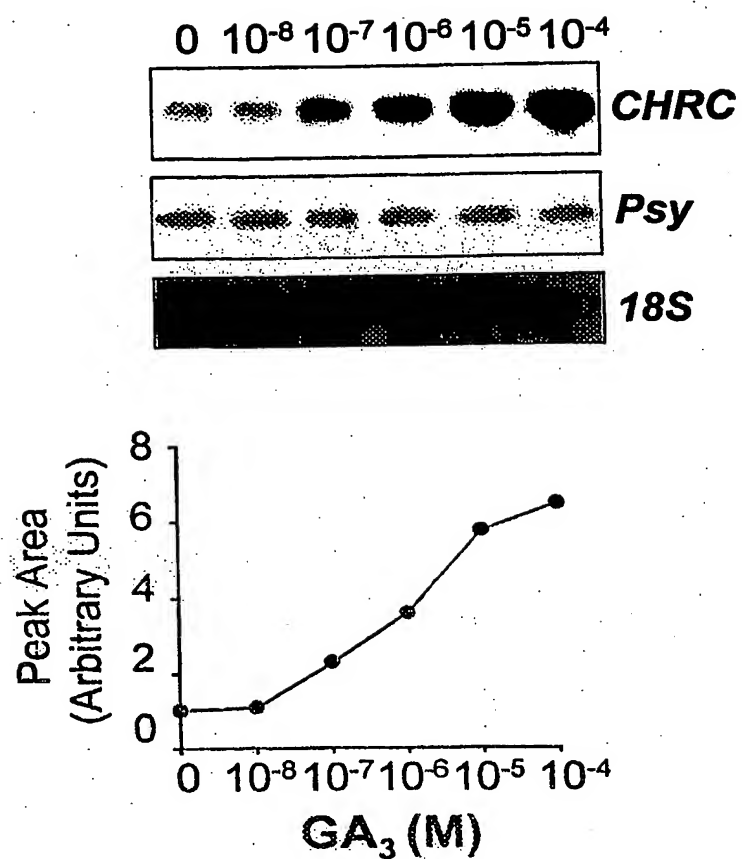


Figure 10

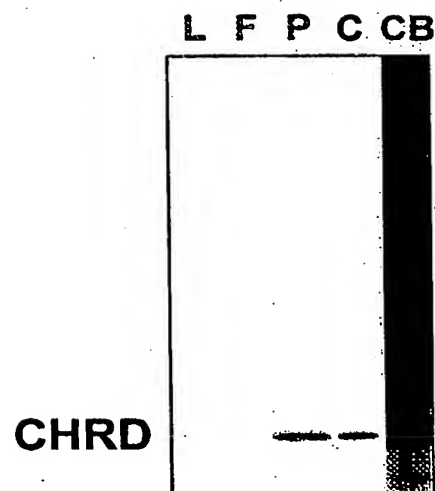


Figure 11

9/11

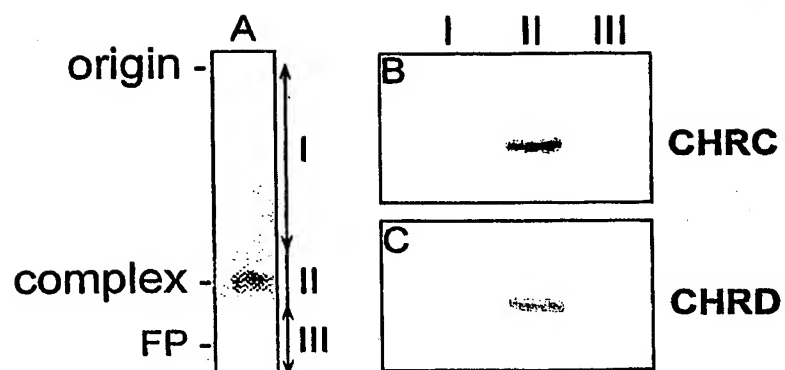


Figure 12

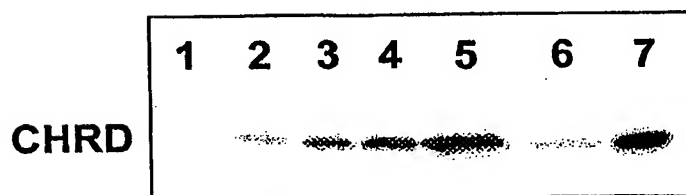


Figure 13

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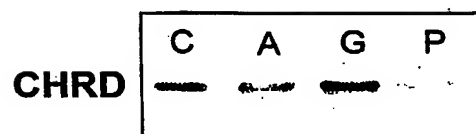


Figure 14A

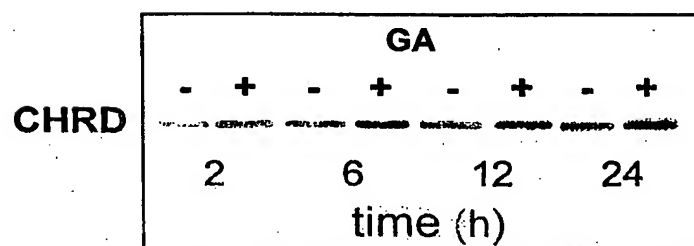


Figure 14B

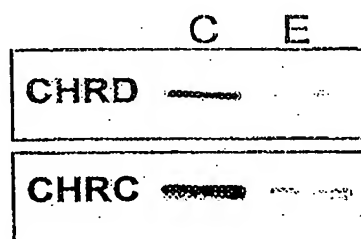


Figure 15A

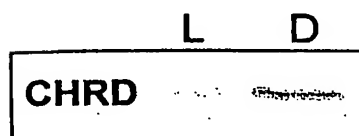


Figure 15B

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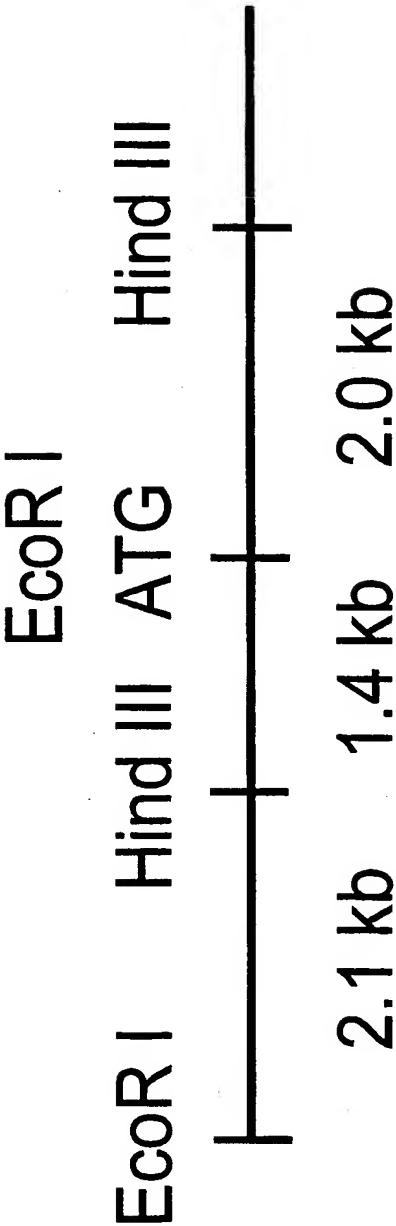


Figure 16

INTERNATIONAL SEARCH REPORT

International application No.
PCT/IL97/00399

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :A01H 1/00; C12N 5/10; A61K 38/16; C07K 14/415; C07H 21/04

US CL :536/24.1, 23.1, 23.6; 800/205; 435/419; 530/324

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/24.1, 23.1, 23.6; 800/205; 435/419; 530/324

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, DIALOG

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 5,429,939 A (MISAWA et al.) 04 July 1995, see entire document, especially Abstract.	8-10

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
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O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

02 MARCH 1998

Date of mailing of the international search report

29 APR 1998

Name and mailing address of the ISA/US
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Authorized officer

PHUONG BUI

Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.
PCT/IL97/00399

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 1-6 and 11
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

Claims 1-6 and 11 are directed to SEQ ID NOs. However, since no computer-readable forms of the sequences were submitted, a sequence search of the claimed sequences on the computer databases cannot be carried out.

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

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